

PRINCIPAL COMPONENT ANALYSIS OF RICE GERMPLASM ACCESSIONS UNDER HIGH TEMPERATURE STRESS

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ABSTRACT

The present investigation was carried out to determine the relationship and genetic diversity among 293 rice germplasm accessions using principal component analysis for high temperature tolerance. In this study, Component 1 had the contribution from the traits viz., panicle exertion, days to 50% flowering and panicle length which accounted 23.35% to the total variability. Total number of tillers, number of productive tillers, biomass and yield has contributed 17.75% to the total variability in component 2. The remaining variability of 17.13%, 9.93% and 9.22% was consolidated in component 3, component 4 and component 5 by various traits like grain length, grain breadth, L/B ratio, hundred grain weight, number of grains per panicle and spikelet sterility. The cumulative variance of 77.38% of total variation among 15 characters was explained by the first five axes. Thus the results of principal component analysis revealed, wide genetic variability exists in this rice germplasm accessions. High temperature tolerant traits with high genetic variability are expected to provide high level of gene transfer during breeding programs.

KEYWORDS: Principal Component Analysis, Rice, High Temperature Tolerance

INTRODUCTION

High temperature (heat) stress is considered to be one of the major environmental factors limiting crop growth and yield. Rice has been cultivated under a wide range of climatic conditions. Almost 90% of the world's rice is grown and consumed in Asia, where 50% of the population depends on rice for food (Tenorio *et al.* 2013). The rise in atmospheric temperature causes detrimental effects on growth, yield and quality of the rice crop by affecting its phenology, physiology and yield components (Sheehy *et al.* 2005, Peng *et al.* 2004, shrivastava *et al.* 2012). The growth of a rice plant can be broadly divided into three phases: vegetative, reproductive and ripening or grain filling (Maclean *et al.* 2002 and Yoshida, 1981).

Wide genetic variability exists in the rice genetic resources for resistance to heat stress (Prasad *et al.*, 2006; Matsui and Omasa, 2002). Genetic diversity for heat tolerance is important for breeding new varieties for areas affected by high temperatures during the rice-growing season. Some heat-tolerant varieties have been identified in previous studies (Satake and Yoshida, 1978; Matsui *et al.*, 1997, 2001; Jagadish *et al.*, 2008; Tenorio *et al.* 2013).

Statistical method of classification is usually by multivariate methods as it has extensive use in summarizing and describing the inherent variation among crop genotypes. Multivariate statistical tools include Principal Component Analysis (PCA), Cluster analysis and discriminate analysis (Oyelola, 2004). Principal Component Analysis (PCA) can be used to uncover similarities between variable and classify the cases (genotypes), while cluster analysis on the other hand is concerned with classifying previously unclassified materials (Leonard and Peter, 2009).

Principal Component Analysis (PCA) is a multivariate technique that analyses a data table in which observations are described by several inter-correlated quantitative dependent variables. Its goal is to extract the important information from the table, to represent it as a set of new orthogonal variables called principal components, and to display the pattern of similarity of the observations and of the variables as points in maps. 'Proper values' measure the importance and contribution of each component to total variance, whereas each coefficient of proper vectors indicates the degree of contribution of every original variable with which each principal component is associated. The higher the coefficients, regardless of the direction (positive or negative), the more effective they will be in discriminating between accessions. The study is aimed to determine level of germplasm variation in rice to identify and classify variation for grouping the accessions by taking into account several characteristics and relationship between them.

MATERIALS AND METHODS

The study was conducted during *Rabi* 2014 at Paddy breeding station, Tamil Nadu Agriculture University, Coimbatore. A total of 293 genetically diverse rice germplasm accessions were laid out in randomized block design with two replications by adopting a spacing of 20x20 cm. All the agronomic package of practices were carried out to ensure healthy plant growth. Observations were recorded on fifteen quantitative high temperature related traits viz., panicle exertion, days to 50 % flowering, plant height, number of tillers per plant, number of productive tillers per plant, hundred grain weight, panicle length, spikelet sterility, number of grains per panicle, total dry matter production, grain length, grain breadth, L/B ratio, grain filling rate and grain yield per plant. The PCA analysis reduces the dimensions of a multivariate data to a few principal axes, generates an Eigen vector for each axis and produces component scores for the characters. (Sneath et al, 1973 and Ariyo et al, 1991).

RESULTS AND DISCUSSIONS

Principal Component Analysis

The result of the PCA explained the genetic diversity of the rice collection. There are no standard tests to prove significance of proper values and the coefficients. Principal component analysis has shown the genetic diversity of the germplasm lines. The cumulative variance of 77.38% (Table 1) by the first five axes with Eigen value of > 1.0 indicates that the identified traits within the axes exhibited great influence on the phenotype of germplasm lines. A scatter plot was drawn between PC1 and PC2 depicted a clear pattern of grouping genotypes in the factor plane. Convex of the hull showing the outliers was occupied by the genotypes namely 6, 12, 107, 109, 164, 224, 233, and 251. All the genotypes were widely scattered across different quarters (Figure 2). In this study, we chose to follow the criterion used by Clifford and Stephenson (1975) and corroborated by Guei *et al.* (2005), which suggested that the first three principal components are often the most important in reflecting the variation patterns among accessions, and the characters associated with these are more useful in differentiating accessions. According to this criterion, the first three components account for more than 58.24 % of total variation giving a clear idea of the structure underlying the variables analysed. However, the criterion of Raji (2002) was chosen to determine the cutoff limit for the coefficients of the proper vectors; this criterion treated coefficients greater than 0.3 as having a large enough effect to be considered important, while traits having a coefficient less than 0.3 were considered not to have important effects on the overall variation observed in the present study.

The distribution of germplasm lines based on first and second principal component exhibits the phenotypic variation among the population and explains how they widely dispersed along both the axes (Figure 1). PCA of quantitative traits found that, the first principal component accounted 23.35 % to the total variability, where by panicle

exertion (0.78), days to flowering (0.47), plant height (0.32) and panicle length (0.81) were contributed positively. The second principal component accounted 17.75 % to the total variability. The variables contributing most positively were total tillers (0.81), productive tillers (0.79), biomass (0.37) and yield (0.36). The third component accounted 17.13% to the variance, in which the variable grain length (0.49), grain breadth (0.60) and L/B ratio (0.82) contributed positively. Fourth principal component accounted 9.93 % of variance in the total variability by hundred grain weight (0.63). The fifth principal component accounted for 9.22% of the total variation. Number of grains per panicle (0.44) and spikelet sterility (0.35) contributed highest in the variation. Thus, the prominent characters coming together in different principal components and contributing towards explaining the variability and have the tendency to remain together. This may be kept into consideration during utilization of these characters in breeding program.

The phenotypic value of the each trait measures the importance and contribution of each component to total variance, whereas each coefficient of proper vectors indicates the degree of contribution of every original variable with which each principal component is associated. The first 5 components accounted for 77.38% of the total variation. Characters with high variability are expected to provide high level of gene transfer during breeding programs (Gana, 2006; Gana, 2013; Varthini, 2014).

CONCLUSIONS

The phenotypic value of the each trait measures the importance and contribution of each component to total variance, whereas each coefficient of proper vectors indicates the degree of contribution of every original variable with which each principal component is associated. Thus, the prominent characters coming together in different principal components and contributing towards explaining the variability and have the tendency to remain together this may be kept into consideration during utilization of these characters in breeding program.

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APPENDICES

Table 1: Eigen Value, Factor Scores and Contribution of the First Six Principal Component Axes to Variation in Rice Genotypes

Parameter	PC1	PC2	PC3	PC4	PC5
Panicle exertion (Days)	0.778	0.003	0.006	0.006	0.014
Plant Height (cm)	0.322	0.000	0.296	0.006	0.020
Days to 50% flowering (No)	0.465	0.000	0.002	0.019	0.069
Total tillers (No)	0.067	0.812	0.000	0.018	0.028
Productive tillers (No)	0.097	0.786	0.001	0.010	0.023
Panicle length (cm)	0.814	0.006	0.006	0.006	0.014

Table 1:Contd.,					
Grains/panicle	0.174	0.003	0.084	0.020	0.441
100 grain weight (g)	0.001	0.169	0.003	0.634	0.002
Spikelet Sterility (%)	0.274	0.008	0.053	0.021	0.348
Biomass (g)	0.271	0.370	0.116	0.024	0.020
Grain length (cm)	0.112	0.006	0.485	0.228	0.007
Grain breadth (cm)	0.031	0.104	0.600	0.116	0.038
L/B Ratio	0.089	0.026	0.816	0.000	0.041
Grain filling rate (g/day)	0.002	0.007	0.017	0.253	0.114
Yield/plant (g)	0.009	0.362	0.085	0.128	0.203
Eigenvalue	3.504	2.663	2.569	1.490	1.383
Variability (%)	23.358	17.751	17.127	9.930	9.217
Cumulative %	23.358	41.110	58.237	68.167	77.384

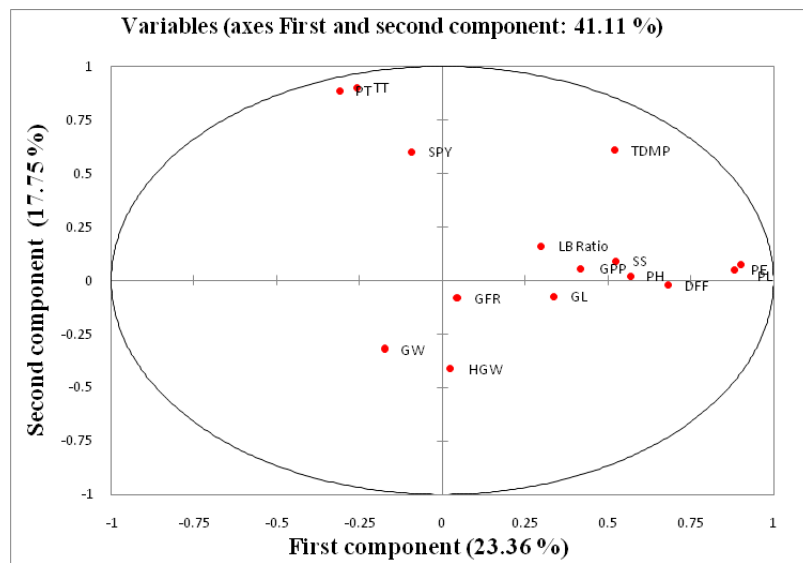


Figure 1: Loading Plot of Phenotypic Heat Tolerance Related Traits in Rice Germplasms

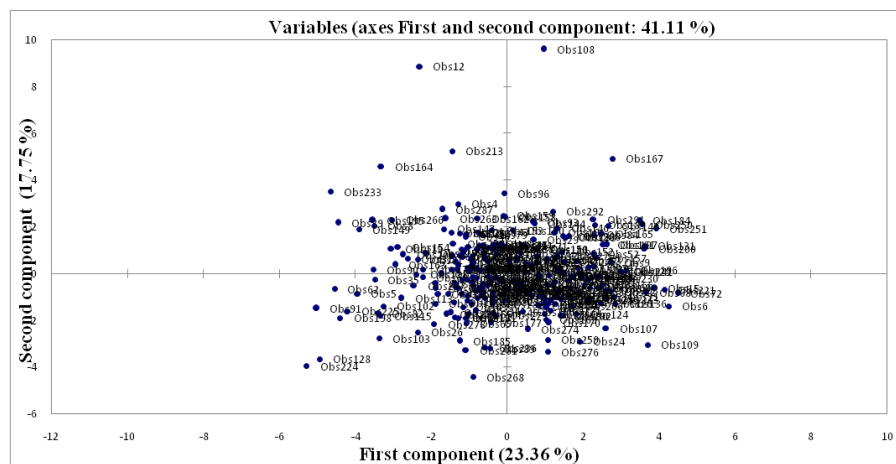


Figure 2: Distribution of Genotypes across Two Components

